#11

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JUN 04 2003
TECH CENTER 1600/2900

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 6/29/2003
Edited by:
Verified by: (STIC Staff)

Serial Number: 10/009,782A

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

1600

RAW SEQUENCE LISTING DATE: 05/29/2003
PATENT APPLICATION: **US/10/009,782A** TIME: 20:56:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05292003\J009782A.raw**

```
      3 <110> APPLICANT: AMANO ENZYME INC.
      4       Takeuchi, Ken-Ichi
      5       Isobe, Kimiyasu
      6       Moriguchi, Mitsuaki
      7       Hirose, Yoshihiko
      8       Koide, Yoshinao
     10 <120> TITLE OF INVENTION: TRANSFORMED MICROORGANISM AND PROCESS FOR PRODUCING D-
AMINOACYLASE
     12 <130> FILE REFERENCE: 217301US-0
     14 <140> CURRENT APPLICATION NUMBER: 10/009,782A
     15 <141> CURRENT FILING DATE: 2002-03-25
     17 <150> PRIOR APPLICATION NUMBER: PCT/JP00/03932
     18 <151> PRIOR FILING DATE: 2000-06-15
     20 <150> PRIOR APPLICATION NUMBER: JAPAN 11/170555
     21 <151> PRIOR FILING DATE: 1999-06-17
     23 <160> NUMBER OF SEQ ID NOS: 3
     25 <170> SOFTWARE: PatentIn version 3.1
     27 <210> SEQ ID NO: 1
     28 <211> LENGTH: 1758
     29 <212> TYPE: DNA
     30 <213> ORGANISM: Alcaligenes xylosoxydans subsp. xylosoxydans
     32 <220> FEATURE:
     33 <221> NAME/KEY: CDS
     34 <222> LOCATION: (34)..(1485)
     35 <223> OTHER INFORMATION:
W--> 37 <400> 1
     38 gaattccact tgatcgcgga aggagagatt tcc atg tcc caa tcc gat tcc cag      54
     39                                     Met Ser Gln Ser Asp Ser Gln
     40                                     1               5
     42 ccc ttc gac ctg ctg ctc gcg ggc ggc acc ctc atc gac ggc agc aac      102
     43 Pro Phe Asp Leu Leu Leu Ala Gly Gly Thr Leu Ile Asp Gly Ser Asn
     44         10                  15                  20
     46 acc ccg ggg cgg cgc gcc gac ctg ggc gtg cgc ggc gac cgc atc gcc      150
     47 Thr Pro Gly Arg Arg Ala Asp Leu Gly Val Arg Gly Asp Arg Ile Ala
     48     25                  30                  35
     50 gcc atc ggc gat ctg tcg gac gcc gcc gcg cac acc cgg gtc gac gtg      198
     51 Ala Ile Gly Asp Leu Ser Asp Ala Ala Ala His Thr Arg Val Asp Val
     52 40                  45                  50                  55
     54 tcg ggc ctg gtg gtc gcg ccc ggc ttc atc gac tcg cac acc cac gac      246
     57 Ser Gly Leu Val Val Ala Pro Gly Phe Ile Asp Ser His Thr His Asp
     58                 60                  65                  70
     60 gac aac tac ctg ctc agg cgt cgc gac atg acg ccc aag atc tcg cag      294
     61 Asp Asn Tyr Leu Leu Arg Arg Arg Asp Met Thr Pro Lys Ile Ser Gln
     62             75                  80                  85
```

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```
64 ggc gtc acc acg gtg gtc acg ggc aat tgc ggc atc agc ctg gcg ccg      342
65 Gly Val Thr Thr Val Val Thr Gly Asn Cys Gly Ile Ser Leu Ala Pro
66         90                  95                  100
68 ctg gcg cac gcc aac ccg ccc gcc ccc ctg gac ctg ctg gac gaa ggc      390
69 Leu Ala His Ala Asn Pro Pro Ala Pro Leu Asp Leu Leu Asp Glu Gly
70     105                 110                 115
72 ggc tct tac cgt ttc gag cgc ttc gcc gac tac ctg gac gcg ttg cgg      438
73 Gly Ser Tyr Arg Phe Glu Arg Phe Ala Asp Tyr Leu Asp Ala Leu Arg
74 120                 125                 130                 135
76 gcc acg ccg gcg gcc gtc aac gcc gcc tgt atg gtg ggc cat tca acg      486
77 Ala Thr Pro Ala Ala Val Asn Ala Ala Cys Met Val Gly His Ser Thr
78                 140                 145                 150
80 ctg cgc gcc gcg gtc atg ccg gac ttg cag cgc gcc gcc acc gac gag      534
81 Leu Arg Ala Ala Val Met Pro Asp Leu Gln Arg Ala Ala Thr Asp Glu
82             155                 160                 165
84 gaa atc gcg gcc atg cgg gac ctg gcc gag gaa gcc atg gcc agc ggc      582
85 Glu Ile Ala Ala Met Arg Asp Leu Ala Glu Glu Ala Met Ala Ser Gly
86         170                 175                 180
88 gcc atc ggc att tcg acc ggc gcc ttc tac ccg ccc gcc gcc cgc gcc      630
89 Ala Ile Gly Ile Ser Thr Gly Ala Phe Tyr Pro Pro Ala Ala Arg Ala
90     185                 190                 195
92 acc acc gaa gag atc atc gag gtg tgc cgg ccg ctg agc gcg cat ggc      678
93 Thr Thr Glu Glu Ile Ile Glu Val Cys Arg Pro Leu Ser Ala His Gly
94 200                 205                 210                 215
96 ggc atc tac gcc acc cac atg cgc gac gaa ggc gag cac atc gtg gcc      726
97 Gly Ile Tyr Ala Thr His Met Arg Asp Glu Gly Glu His Ile Val Ala
98                 220                 225                 230
100 gcg ctg gag gaa acc ttc cgc atc ggc cgc gag ctg gac gtg ccg gtg      774
101 Ala Leu Glu Glu Thr Phe Arg Ile Gly Arg Glu Leu Asp Val Pro Val
102             235                 240                 245
104 gtg atc tcg cac cac aag gtc atg ggc cag ccc aat ttc ggc cgc tcg      822
105 Val Ile Ser His His Lys Val Met Gly Gln Pro Asn Phe Gly Arg Ser
106         250                 255                 260
108 cgc gag acg ctg ccg ctg atc gag gcc gcc atg gcg cgc cag gac gtc      870
111 Arg Glu Thr Leu Pro Leu Ile Glu Ala Ala Met Ala Arg Gln Asp Val
112     265                 270                 275
114 tcg ctg gac gcg tat ccc tac gtg gcc ggc tcc acc atg ctc aag cag      918
115 Ser Leu Asp Ala Tyr Pro Tyr Val Ala Gly Ser Thr Met Leu Lys Gln
116 280                 285                 290                 295
118 gac cgc gtg ctg ctg gcc gga cgc acc atc atc acc tgg tgc aag ccc      966
119 Asp Arg Val Leu Leu Ala Gly Arg Thr Ile Ile Thr Trp Cys Lys Pro
120                 300                 305                 310
122 ttc ccc gaa ctg agc ggg cgc gac ctg gat gaa gtc gcg gcc gag cgc     1014
123 Phe Pro Glu Leu Ser Gly Arg Asp Leu Asp Glu Val Ala Ala Glu Arg
124             315                 320                 325
126 ggc aaa tcc aag tac gac gtg gtg ccc gag ctg cag ccg gcc ggc gcc     1062
127 Gly Lys Ser Lys Tyr Asp Val Val Pro Glu Leu Gln Pro Ala Gly Ala
128         330                 335                 340
130 atc tac ttc atg atg gac gaa ccc gac gtg cag cgc atc ctg gcg ttc     1110
```

RAW SEQUENCE LISTING DATE: 05/29/2003
PATENT APPLICATION: **US/10/009,782A** TIME: 20:56:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05292003\J009782A.raw**

```
131 Ile Tyr Phe Met Met Asp Glu Pro Asp Val Gln Arg Ile Leu Ala Phe
132     345                 350                 355
134 ggc ccg acc atg atc ggc tcc gac ggc ctg ccg cac gac gag cgc ccg     1158
135 Gly Pro Thr Met Ile Gly Ser Asp Gly Leu Pro His Asp Glu Arg Pro
136 360                 365                 370                 375
138 cat ccg cgc ctg tgg ggc acc ttc ccg cgg gtg ctg ggg cac tat gcg     1206
139 His Pro Arg Leu Trp Gly Thr Phe Pro Arg Val Leu Gly His Tyr Ala
140                 380                 385                 390
142 cgc gac ctg ggc ctg ttc ccg ctg gag acg gcg gta tgg aag atg acc     1254
143 Arg Asp Leu Gly Leu Phe Pro Leu Glu Thr Ala Val Trp Lys Met Thr
144             395                 400                 405
146 ggc ctg acc gcc gcg cgc ttc ggc ctg gcc ggg cgc ggg cag ctg cag     1302
147 Gly Leu Thr Ala Ala Arg Phe Gly Leu Ala Gly Arg Gly Gln Leu Gln
148         410                 415                 420
150 gcc ggg tac ttc gcc gac ctg gtg gtg ttc gac ccg gcc acg gtg gcc     1350
151 Ala Gly Tyr Phe Ala Asp Leu Val Val Phe Asp Pro Ala Thr Val Ala
152     425                 430                 435
154 gat acc gcc acc ttc gaa cac cct acc gag cgc gcc gcc ggc atc cat     1398
155 Asp Thr Ala Thr Phe Glu His Pro Thr Glu Arg Ala Ala Gly Ile His
156 440                 445                 450                 455
158 tcc gtg tac gtc aac ggc gcg ccg gtc tgg caa gag cag gcg ttc acc     1446
159 Ser Val Tyr Val Asn Gly Ala Pro Val Trp Gln Glu Gln Ala Phe Thr
160                 460                 465                 470
162 ggc cag cat gcc ggc cgc gtg ctc gca cgc acg gcc gcc tgagcccggc     1495
165 Gly Gln His Ala Gly Arg Val Leu Ala Arg Thr Ala Ala
166             475                 480
168 gccagccctt acaatccggc gtgaacgggg cggcgtgccg ccccctccca accctggacg   1555
170 caaaccgcta catggccccc ccctccgctc gcaatacggc cccacccgat atcgtgggca   1615
172 aggaagtgat gggcgcgcgc ctgcgcgccg agcgcaaggc ccggaaaatg accctgcaag   1675
174 acctgtcgca ggccagcggc atcgcggtct cgaccctgtc caaggccgag ctgggccaga   1735
176 tcgccctgag ctacgagaag ctt                                         1758
179 <210> SEQ ID NO: 2
180 <211> LENGTH: 484
181 <212> TYPE: PRT
182 <213> ORGANISM: Alcaligenes xylosoxydans subsp. xylosoxydans
184 <400> SEQUENCE: 2
186 Met Ser Gln Ser Asp Ser Gln Pro Phe Asp Leu Leu Leu Ala Gly Gly
187 1               5                   10                  15
190 Thr Leu Ile Asp Gly Ser Asn Thr Pro Gly Arg Arg Ala Asp Leu Gly
191             20                  25                  30
194 Val Arg Gly Asp Arg Ile Ala Ala Ile Gly Asp Leu Ser Asp Ala Ala
195         35                  40                  45
198 Ala His Thr Arg Val Asp Val Ser Gly Leu Val Val Ala Pro Gly Phe
199     50                  55                  60
202 Ile Asp Ser His Thr His Asp Asp Asn Tyr Leu Leu Arg Arg Arg Asp
203 65                  70                  75                  80
206 Met Thr Pro Lys Ile Ser Gln Gly Val Thr Thr Val Val Thr Gly Asn
207                 85                  90                  95
210 Cys Gly Ile Ser Leu Ala Pro Leu Ala His Ala Asn Pro Pro Ala Pro
```

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PATENT APPLICATION: **US/10/009,782A** TIME: 20:56:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05292003\J009782A.raw**

```
211                 100                 105                 110
214 Leu Asp Leu Leu Asp Glu Gly Gly Ser Tyr Arg Phe Glu Arg Phe Ala
215         115                 120                 125
219 Asp Tyr Leu Asp Ala Leu Arg Ala Thr Pro Ala Ala Val Asn Ala Ala
220     130                 135                 140
223 Cys Met Val Gly His Ser Thr Leu Arg Ala Ala Val Met Pro Asp Leu
224 145                 150                 155                 160
227 Gln Arg Ala Ala Thr Asp Glu Glu Ile Ala Ala Met Arg Asp Leu Ala
228                 165                 170                 175
231 Glu Glu Ala Met Ala Ser Gly Ala Ile Gly Ile Ser Thr Gly Ala Phe
232             180                 185                 190
235 Tyr Pro Pro Ala Ala Arg Ala Thr Thr Glu Glu Ile Ile Glu Val Cys
236         195                 200                 205
239 Arg Pro Leu Ser Ala His Gly Gly Ile Tyr Ala Thr His Met Arg Asp
240     210                 215                 220
243 Glu Gly Glu His Ile Val Ala Ala Leu Glu Glu Thr Phe Arg Ile Gly
244 225                 230                 235                 240
247 Arg Glu Leu Asp Val Pro Val Val Ile Ser His His Lys Val Met Gly
248                 245                 250                 255
251 Gln Pro Asn Phe Gly Arg Ser Arg Glu Thr Leu Pro Leu Ile Glu Ala
252             260                 265                 270
255 Ala Met Ala Arg Gln Asp Val Ser Leu Asp Ala Tyr Pro Tyr Val Ala
256         275                 280                 285
259 Gly Ser Thr Met Leu Lys Gln Asp Arg Val Leu Leu Ala Gly Arg Thr
260     290                 295                 300
263 Ile Ile Thr Trp Cys Lys Pro Phe Pro Glu Leu Ser Gly Arg Asp Leu
264 305                 310                 315                 320
267 Asp Glu Val Ala Ala Glu Arg Gly Lys Ser Lys Tyr Asp Val Val Pro
268                 325                 330                 335
273 Glu Leu Gln Pro Ala Gly Ala Ile Tyr Phe Met Met Asp Glu Pro Asp
274             340                 345                 350
277 Val Gln Arg Ile Leu Ala Phe Gly Pro Thr Met Ile Gly Ser Asp Gly
278         355                 360                 365
281 Leu Pro His Asp Glu Arg Pro His Pro Arg Leu Trp Gly Thr Phe Pro
282     370                 375                 380
285 Arg Val Leu Gly His Tyr Ala Arg Asp Leu Gly Leu Phe Pro Leu Glu
286 385                 390                 395                 400
289 Thr Ala Val Trp Lys Met Thr Gly Leu Thr Ala Ala Arg Phe Gly Leu
290                 405                 410                 415
293 Ala Gly Arg Gly Gln Leu Gln Ala Gly Tyr Phe Ala Asp Leu Val Val
294             420                 425                 430
297 Phe Asp Pro Ala Thr Val Ala Asp Thr Ala Thr Phe Glu His Pro Thr
298         435                 440                 445
301 Glu Arg Ala Ala Gly Ile His Ser Val Tyr Val Asn Gly Ala Pro Val
302     450                 455                 460
305 Trp Gln Glu Gln Ala Phe Thr Gly Gln His Ala Gly Arg Val Leu Ala
306 465                 470                 475                 480
309 Arg Thr Ala Ala
```

313 <210> SEQ ID NO: 3

RAW SEQUENCE LISTING DATE: 05/29/2003
PATENT APPLICATION: **US/10/009,782A** TIME: 20:56:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05292003\J009782A.raw**

314 <211> LENGTH: 6
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Nucleotide sequence in ribosome binding site for improving translation
320 efficiency.
322 <400> SEQUENCE: 3
323 gaagga 6

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/29/2003
PATENT APPLICATION: **US/10/009,782A** TIME: 20:56:36

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05292003\J009782A.raw**

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3

VERIFICATION SUMMARY DATE: 05/29/2003
PATENT APPLICATION: **US/10/009,782A** TIME: 20:56:36

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05292003\J009782A.raw**

L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35